

5000

II9

PCT09

3.5.8.8 B

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,876

DATE: 06/27/2001

TIME: 15:06:32

Input Set : A:\Rutgers White ('876) Sequence Listing.txt

Output Set: N:\CRF3\06272001\I674876.raw

ENTERED

over
8/2/01

3 <110> APPLICANT: White, Eileen
 4 Kasof, Gary
 5 Goyal, Lakshmi
 6 Rutgers, The State University of New Jersey
 8 <120> TITLE OF INVENTION: Recombinant Cell Line and Screening
 9 Method for Identifying Agents Which Regulate Apoptosis and
 10 Tumor Suppression
 12 <130> FILE REFERENCE: Rut-98-0058
 14 <140> CURRENT APPLICATION NUMBER: 09/674,876
 C--> 15 <141> CURRENT FILING DATE: 2001-05-31
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/09793
 18 <151> PRIOR FILING DATE: 1999-05-06
 20 <150> PRIOR APPLICATION NUMBER: 60/084,664
 21 <151> PRIOR FILING DATE: 1998-05-07
 23 <160> NUMBER OF SEQ ID NOS: 2
 25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 2610
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo Sapiens
 33 <400> SEQUENCE: 1

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35	tctcgatcaa	gatcaagatc	tcattctaga	aagaagcgat	acaggtctcg	ttccagaaca	120
36	tattcaaggt	ctogtagtag	agatcgtag	tattctagag	attatcgtag	cgattacaga	180
37	aataatagag	gaatgagacg	accttatggg	tacagaggaa	ggggtagagg	gtattatcaa	240
38	ggaggaggag	gtagatatca	tcgaggtggg	tatagacctg	tctggaatag	aaggcactct	300
39	aggagtccta	gacgaggtcg	ttcacgttcc	aggagtccaa	aaagaagatc	cgtttcttct	360
40	caaagatcca	gaagcagatc	tcgccgggtc	tatagatctt	ctaggtctcc	aagatcatcc	420
41	tcttctcggt	cttcatcccc	atatagcaaa	tctcctgttt	ctaaaagacg	agggctctcag	480
42	gaaaaacaaa	ccaaaaaagc	tgaaggggaa	ccccaagaag	agagtcctgt	gaaaagtaaa	540
43	tcacaggagg	aaccgaaaga	tacatttgaa	catgacccat	ctgagtctat	cgatgaattt	600
44	aataagtcac	cagccacatc	cggtgatatt	tggcctggcc	tttcagctta	tgataaatgt	660
45	cctagatcac	cccatagtcc	ttcacctatt	gctacaccac	ctagtcagag	ttcatcttgc	720
46	tctgatgctc	ccatgctcag	tacagttcac	tctgcaaaaa	atactccttc	tcagcattca	780
47	cattccattc	agcatagtcc	tgaaaggtct	gggtctgggt	ctggttgaaa	tggatctagt	840
48	cgatacagtc	cttctcagaa	tagtccaatt	catcacatcc	cttcacgaag	aagtcctgca	900
49	aagacaatcg	caccacagaa	tgctccaaga	gatgagtcta	ggggccgttc	ctcgttttat	960
50	cctgatgggt	gagatcagga	aactgcaaa	actgggaagt	tcttaaaaa	gttcacagat	1020
51	gaagagtcta	gagtattcct	gcttgatagg	ggtaatacca	gggataaaga	ggcttcaaaa	1080
52	gagaaaggat	catagaaagg	gagggcagag	ggagaatggg	aagatcagga	agctctagat	1140
53	tacttcagtg	ataaagagtc	tggaaaacaa	aagtttaatg	attcagaagg	ggatgacaca	1200
54	gaggagacag	aggattatag	acagttcagg	aagtcagtcc	tcgcagatca	gggtaaaagt	1260
55	tttgctactg	catctcaccg	gaatactgag	gaggaaggac	tcaagtacaa	gtccaaagtt	1320
56	tactgaaaag	gcaatagaga	aagtgatgga	tttagagaag	aaaaaaatta	taaaacttaa	1380
57	gagactggat	atgtagtgga	aaggcctagc	actacaaaag	ataagcacia	agaagaagac	1440
58	aaaaattctg	aaagaataac	agtaaagaaa	gaaactcagt	cacctgagca	ggtaaagtct	1500
59	gaaaagctca	aagacctctt	tgattacagt	ccccctctac	acaagaatct	ggatgcacga	1560

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60 gaaaagtcta ccttcagaga ggaaagccca cttaggatca aaatgatagc gagtgattct 1620
61 caccgtcctg aagtcaaact caaaatggca cctgttcctc ttgatgattc taacagacct 1680
62 gcttccttga ctaaagacag gctgcttgct agtacacttg tccattctgt caagaaggag 1740
63 caagaattcc gatccatctt tgaccacatt aagttgccac aggccagcaa aagcacttca 1800
64 gagtcattta ttcaacacat tgtgtccttg gttcatcatg ttaaagagca atacttcaag 1860
65 tcagctgcaa tgaccctaaa cgagcgggttc acttcgtatc agaaagccac tgaagaacat 1920
66 agtactcggc aaaagagccc tgaatacac aggagaattg acatctcacc aagtaccctg 1980
67 aggaagcata cccgttttagc aggggaagag agagttttta aagaagaaaa tcaaaaggga 2040
68 gataaaaaat taaggtgtga ctctgctgac cttcggcatg acattgatcg ccgtagaaaa 2100
69 gaaagaagta aagaacgggg agattccaag ggctccaggg aatccagtgg atcaagaaag 2160
70 caggaaaaaa ctccaaaaga ttacaaggaa tacaatctt acaaagatga cagtaaacad 2220
71 aaaagagagc aagatcattc tcgatcttca tcctcttcag catcaccttc ttctcccagt 2280
72 tctcgagaag aaaaggagag taagaaggaa agagaagaag aatttaaaac tcaccatgaa 2340
73 atgaaagaat actcaggctt tgcaggagtt agccgaccac gaggaacctt tcatgacgac 2400
74 agagatgatg gtgtggatta ttgggccaac agaggaagag gtcgtggtac ttttcaacgt 2460
75 ggcagagggc gctttaactt caaaaatatc ggtagcagtc ctaaatggac tcatgacaaa 2520
76 taccaagggg atgggattgt tgaagatgaa gaagagacca tggaaaataa tgaagaaaag 2580
77 aaggacagac gcaaggaaga aaaggaataa

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80 <210> SEQ ID NO: 2

81 <211> LENGTH: 917

82 <212> TYPE: PRT

83 <213> ORGANISM: Homo sapiens

85 <400> SEQUENCE: 2

```

86 Met Gly Arg Ala Asn Ser Arg Ser His Ser Ser Arg Ser Lys Ser Arg
87 1 5 10 15
88 Ser Gln Ser Ser Ser Arg Ser Arg Ser Arg Ser His Ser Arg Lys Lys
89 20 25 30
90 Arg Tyr Arg Ser Arg Ser Arg Thr Tyr Ser Arg Ser Arg Ser Arg Asp
91 35 40 45
92 Arg Met Tyr Ser Arg Asp Tyr Arg Arg Asp Tyr Arg Asn Asn Arg Gly
93 50 55 60
94 Met Arg Arg Pro Tyr Gly Tyr Arg Gly Arg Gly Arg Gly Tyr Tyr Gln
95 65 70 75 80
96 Gly Gly Gly Gly Arg Tyr His Arg Gly Gly Tyr Arg Pro Val Trp Asn
97 85 90 95
98 Arg Arg His Ser Arg Ser Pro Arg Arg Gly Arg Ser Arg Ser Arg Ser
99 100 105 110
100 Pro Lys Arg Arg Ser Val Ser Ser Arg Ser Arg Ser Arg Ser Arg Arg
101 115 120 125
102 Ser Tyr Arg Ser Ser Arg Ser Pro Arg Ser Ser Ser Ser Arg Ser Ser
103 130 135 140
104 Ser Pro Tyr Ser Lys Ser Pro Val Ser Lys Arg Arg Gly Ser Gln Glu
105 145 150 155 160
106 Lys Gln Thr Lys Lys Ala Glu Gly Glu Pro Gln Glu Glu Ser Pro Leu
107 165 170 175
108 Lys Ser Lys Ser Gln Glu Glu Pro Lys Asp Thr Phe Glu His Asp Pro
109 180 185 190
110 Ser Glu Ser Ile Asp Glu Phe Asn Lys Ser Ser Ala Thr Ser Gly Asp
111 195 200 205

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```

112 Ile Trp Pro Gly Leu Ser Ala Tyr Asp Asn Ser Pro Arg Ser Pro His
113      210                      215                      220
114 Ser Pro Ser Pro Ile Ala Thr Pro Pro Ser Gln Ser Ser Ser Cys Ser
115      225                      230                      235                      240
116 Asp Ala Pro Met Leu Ser Thr Val His Ser Ala Lys Asn Thr Pro Ser
117      245                      250                      255
118 Gln His Ser His Ser Ile Gln His Ser Pro Glu Arg Ser Gly Ser Gly
119      260                      265                      270
120 Ser Val Gly Asn Gly Ser Ser Arg Tyr Ser Pro Ser Gln Asn Ser Pro
121      275                      280                      285
122 Ile His His Ile Pro Ser Arg Arg Ser Pro Ala Lys Thr Ile Ala Pro
123      290                      295                      300
124 Gln Asn Ala Pro Arg Asp Glu Ser Arg Gly Arg Ser Ser Phe Tyr Pro
125      305                      310                      315                      320
127 Asp Gly Gly Asp Gln Glu Thr Ala Lys Thr Gly Lys Phe Leu Lys Arg
128      325                      330                      335
129 Phe Thr Asp Glu Glu Ser Arg Val Phe Leu Leu Asp Arg Gly Asn Thr
130      340                      345                      350
131 Arg Asp Lys Glu Ala Ser Lys Glu Lys Gly Ser Glu Lys Gly Arg Ala
132      355                      360                      365
133 Glu Gly Glu Trp Glu Asp Gln Glu Ala Leu Asp Tyr Phe Ser Asp Lys
134      370                      375                      380
135 Glu Ser Gly Lys Gln Lys Phe Asn Asp Ser Glu Gly Asp Asp Thr Glu
136      385                      390                      395                      400
137 Glu Thr Glu Asp Tyr Arg Gln Phe Arg Lys Ser Val Leu Ala Asp Gln
138      405                      410                      415
139 Gly Lys Ser Phe Ala Thr Ala Ser His Arg Asn Thr Glu Glu Glu Gly
140      420                      425                      430
141 Leu Lys Tyr Lys Ser Lys Val Ser Leu Lys Gly Asn Arg Glu Ser Asp
142      435                      440                      445
143 Gly Phe Arg Glu Glu Lys Asn Tyr Lys Leu Lys Glu Thr Gly Tyr Val
144      450                      455                      460
145 Val Glu Arg Pro Ser Thr Lys Asp Lys His Lys Glu Glu Asp Lys
146      465                      470                      475                      480
147 Asn Ser Glu Arg Ile Thr Val Lys Lys Glu Thr Gln Ser Pro Glu Gln
148      485                      490                      495
149 Val Lys Ser Glu Lys Leu Lys Asp Leu Phe Asp Tyr Ser Pro Pro Leu
150      500                      505                      510
151 His Lys Asn Leu Asp Ala Arg Glu Lys Ser Thr Phe Arg Glu Glu Ser
152      515                      520                      525
153 Pro Leu Arg Ile Lys Met Ile Ala Ser Asp Ser His Arg Pro Glu Val
154      530                      535                      540
155 Lys Leu Lys Met Ala Pro Val Pro Leu Asp Asp Ser Asn Arg Pro Ala
156      545                      550                      555                      560
157 Ser Leu Thr Lys Asp Arg Leu Leu Ala Ser Thr Leu Val His Ser Val
158      565                      570                      575
159 Lys Lys Glu Gln Glu Phe Arg Ser Ile Phe Asp His Ile Lys Leu Pro
160      580                      585                      590
161 Gln Ala Ser Lys Ser Thr Ser Glu Ser Phe Ile Gln His Ile Val Ser

```

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162		595		600		605											
163	Leu	Val	His	His	Val	Lys	Glu	Gln	Tyr	Phe	Lys	Ser	Ala	Ala	Met	Thr	
164		610					615					620					
165	Leu	Asn	Glu	Arg	Phe	Thr	Ser	Tyr	Gln	Lys	Ala	Thr	Glu	Glu	His	Ser	
166		625					630				635				640		
167	Thr	Arg	Gln	Lys	Ser	Pro	Glu	Ile	His	Arg	Arg	Ile	Asp	Ile	Ser	Pro	
168					645					650					655		
169	Ser	Thr	Leu	Arg	Lys	His	Thr	Arg	Leu	Ala	Gly	Glu	Glu	Arg	Val	Phe	
170				660					665					670			
171	Lys	Glu	Glu	Asn	Gln	Lys	Gly	Asp	Lys	Lys	Leu	Arg	Cys	Asp	Ser	Ala	
172			675					680					685				
173	Asp	Leu	Arg	His	Asp	Ile	Asp	Arg	Arg	Arg	Lys	Glu	Arg	Ser	Lys	Glu	
174		690					695					700					
175	Arg	Gly	Asp	Ser	Lys	Gly	Ser	Arg	Glu	Ser	Ser	Gly	Ser	Arg	Lys	Gln	
176		705				710					715					720	
177	Glu	Lys	Thr	Pro	Lys	Asp	Tyr	Lys	Glu	Tyr	Lys	Ser	Tyr	Lys	Asp	Asp	
178					725				730						735		
179	Ser	Lys	His	Lys	Arg	Glu	Gln	Asp	His	Ser	Arg	Ser	Ser	Ser	Ser	Ser	
180				740					745					750			
181	Ala	Ser	Pro	Ser	Ser	Pro	Ser	Ser	Arg	Glu	Glu	Lys	Glu	Ser	Lys	Lys	
182			755					760					765				
183	Glu	Arg	Glu	Glu	Glu	Phe	Lys	Thr	His	His	Glu	Met	Lys	Glu	Tyr	Ser	
184		770				775					780						
185	Gly	Phe	Ala	Gly	Val	Ser	Arg	Pro	Arg	Gly	Thr	Phe	Phe	Arg	Ile	Arg	
186		785				790				795						800	
187	Gly	Arg	Gly	Arg	Ala	Arg	Gly	Val	Phe	Ala	Gly	Thr	Asn	Thr	Gly	Pro	
188					805				810						815		
190	Asn	Asn	Ser	Asn	Thr	Thr	Phe	Gln	Lys	Arg	Pro	Lys	Glu	Glu	Glu	Trp	
191				820					825					830			
192	Asp	Pro	Glu	Tyr	Thr	Pro	Lys	Ser	Lys	Lys	Tyr	Phe	Leu	His	Asp	Asp	
193			835					840					845				
194	Arg	Asp	Asp	Gly	Val	Asp	Tyr	Trp	Ala	Lys	Arg	Gly	Arg	Gly	Arg	Gly	
195		850				855					860						
196	Thr	Phe	Gln	Arg	Gly	Arg	Gly	Arg	Phe	Asn	Phe	Lys	Lys	Ser	Gly	Ser	
197		865				870				875						880	
198	Ser	Pro	Lys	Trp	Thr	His	Asp	Lys	Tyr	Gln	Gly	Asp	Gly	Ile	Val	Glu	
199					885				890						895		
200	Asp	Glu	Glu	Glu	Thr	Met	Glu	Asn	Asn	Glu	Glu	Lys	Lys	Asp	Arg	Arg	
201				900				905						910			
202	Lys	Glu	Glu	Lys	Glu												
203				915													

VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date